



Get for ? Site search

EBI Home About EBI Research Services Toolbox Databases Downloads

DATABASE BROWSING

EBI Dbfetch

ID CHCLOSI standard; genomic DNA; PRO; 2768 BP.

XX

AC X63673;

XX

SV X63673.1

XX

DT 21-FEB-1992 (Rel. 31, Created)

DT 19-JUL-1993 (Rel. 36, Last updated, Version 12)

XX

DE *C. histolyticum* closI gene for alpha-clostripain

XX

KW closI gene; Clostripain.

XX

OS *Clostridium histolyticum*

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC *Clostridium*.

XX

RN [1]

RP 1-2368

RA Diefenthal T.;

RT ;

RL Submitted (28-JAN-1992) to the EMBL/GenBank/DDJB databases.

RL T. Diefenthal, Weissheimer Research, Dept. Biotechnology, Schaarstr.1,

RL P.O.B. 20 65, W-5470 Andernach, FRG

XX

RN [2]

RP 1-2368

RX DOI: [10.1007/BF00276893](https://doi.org/10.1007/BF00276893)

RX MEDLINE: 93341452.

RX PUBMED: 8341259.

RA Dargatz H., Diefenthal T., Witte V., Reipen G., von Wettstein D.;

RT "The heterodimeric protease clostripain from *Clostridium histolyticum* is

RT encoded by a single gene";

RL Mol. Genet. 240(1):140-145(1993).

XX

FH	Key	Location/Qualifiers
FT	<u>source</u>	1..2768
FT		/db_xref="taxon:1498"
FT		/mol_type="genomic DNA"
FT		/organism="Clostridium histolyticum"
FT	<u>-35 signal</u>	376..381
FT	<u>-10 signal</u>	397..402
FT	<u>repeat region</u>	420..438
FT		/note="palindrom-structure"
FT		/rpt_type=INVERTED
FT	<u>RBS</u>	605..609
FT	<u>CDS</u>	618..2198
FT		/db_xref="GOA:P09870"
FT		/db_xref="UniProt/Swiss-Prot:P09870"
FT		/transl_table=11
FT		/gene="ClosI"
FT		/EC_number="3.4.22.8"

FT /product="clostripain"
 FT /protein_id="CAA45212.1"
 FT /translation="MLRRKVSTLLMTALITTSFLNSKPVYANPVTKSKDNNLKEVQQVT
 FT SKSNKNKNQKVTIMYYCADCNNLEGSLLNDIEEMKTGYKDSPNLNLI
 FT ALVDRSPRYSSD
 FT EKVLGEDFS DTRLYKIEHNKANRLDGKNEFPEISTTSKYEANMGDPEV
 FT LKKFIDYCKSN
 FT YEADKYVLIMANHGGGAREKSNPRLNRAICWDDSNLDKNGEADCLY
 FT MG EISDHLT
 FT EKNS
 FT VDLIAFDACIMGTAEVAYQYRPGNGGSADTLVASSP
 FT VVWPGPF
 FT KYDKIFDRIKAGGGT
 FT NNEDDLT
 FT LGGKEQNFD
 FT PATITNEQLGALFV
 FT EYQD
 FT STHANGRYDQHLSFYDLKK
 FT AESVK
 FT RAIDNLAVNLS
 FT SENKKS
 FT EIEKL
 FT RGS
 FT GIHTD
 FT LMYF
 FT DEY
 FT ESE
 FT GEW
 FT V
 FT EY
 FT P
 FT FDV
 FT YDLCE
 FT KIN
 KSEN
 KTKD
 LASN
 AMNK
 LNEM
 IVY
 SFG
 DPS
 SNN
 FEG
 KNG
 GLS
 IFL
 P
 GDK
 KY
 ST
 YY
 TKI
 PHWT
 MQSW
 YNS
 IDTV
 KYGL
 NPY
 GK
 LS
 WCKD
 GQD
 PE
 E
 INK
 VGN
 WF
 ELL
 D
 SWF
 D
 K
 T
 NDV
 T
 GGG
 VNH
 YQW"

XX

SQ Sequence 2768 BP; 1084 A; 359 C; 427 G; 898 T; 0 other;

gctataatca	atgcccata	tataaagatt	aaagtaatct	tttgtatcat	ctaataatgg	60
agatcagct	ttattaatta	attgcttttt	taaaaaaatta	ttttaagtt	agtataactct	120
tctactaaat	agttaaattc	agcttttcat	ttttccatca	ctaccataat	tacgtaatca	180
ttatatacata	gaatgctttt	accacgtaat	ataaaaaagca	agagtcctat	attaaatatcc	240
tgaacctaaa	gacctaataatgt	agatttttaa	caaaaacaaat	gattgatcac	ttaatataatc	300
taacagttca	gataacttcc	ttttttagat	tgtatataat	aagtaaattc	aaagaccata	360
aaatataaccc	cccgattgta	atgcttgaat	attaattata	atgaaattat	agtttaaattt	420
aaaaaaataa	tttttttag	aagtttaaga	aggattatcc	taaacattat	agaatataatt	480
aaatataaaa	ataatgtaaa	actttaaata	ataactctt	taatgtaca	taatgtattt	540
atatggatta	aattttaaatt	tatagatgt	ataaaactat	aaattaaatt	aaaatataac	600
tttggaggt	atgttattatg	ttaagaagaa	aagtatcaac	actattatg	acagctttga	660
taactacttc	atttttaaat	tccaaacccg	tatatgcaaa	tccagtaact	aatccaagg	720
ataataactt	aaaagaagta	caacaagtt	caagcaagag	taataaaaac	aaaatcaaa	780
aagtaactat	tatgtactat	tgcgacgcag	acaataactt	ggaaggaagt	ctattaaatg	840
atatcgagga	aatgaaaaaca	ggatataagg	atagtcctaa	tttaattta	attgctcttg	900
tagacagatc	cccaagatat	agcagtgacg	aaaaagttt	aggtgaagat	tttagtgcata	960
cacgtcttta	taagattgaa	cacaataagg	caaataagatt	agacggtaaa	aatgaatttc	1020
cagaaataag	tactactatg	aaatatgaag	ctaacatggg	ggatcctgaa	gttctaaaaa	1080
aatttattga	ttattgtaaa	tctaattatg	aggctgataa	atatgtgcct	ataatggcta	1140
atcatggtgg	ttgtgcagg	gaaaaatcaa	atccaagatt	aaatagagca	atttgcgtgg	1200
atgatagtaa	ccttgataaa	aatggtgaag	cagactgcct	ttatatgggt	gaaatttcag	1260
atcatttaac	agaaaaaaca	tcaatgtt	tacttgcctt	tgatgcattc	tttatgggaa	1320
ctgcagaagt	agcgtatcag	tatagaccag	gtaatggagg	attttctgcc	gatactttag	1380
ttgcttcaag	cccagtagtt	tgggtcctg	gattcaata	tgataagatt	ttcgatagga	1440
taaaagctgg	tggaggaact	aataatgagg	atgatthaac	tttaggtgg	aaagaacaaa	1500
actttgatcc	tgcaaccatt	accaatgagc	aatttaggtgc	attatttgc	gaagagcaaa	1560
gagactcaac	acatgccaat	ggtcgctatg	atcaacactt	aagctttat	gatttaaaga	1620
aagctgaatc	agtaaaaaa	gccatagata	atttagctgt	taatctaagt	aatgaaaaca	1680
aaaaatctga	aattgaaaaa	ttaagaggaa	gtgaaattca	tacagattt	atgcattact	1740
tcgatgaata	ttctgaagga	gaatgggtt	aatatccctt	tttgcacgt	tatgatttt	1800
gtgaaaaaat	aaataaaaatg	gaaaatttt	gtagtaaaac	taaagattt	gcttcaaatt	1860
ctatgaataa	attaaatgaa	atgatgttt	attcttttg	agacccctgt	ataatatttt	1920
aagaaggaaa	aatggattt	agtatattct	tacctaattt	agataaaaaa	tattcaactt	1980
attatacattc	aaccaagata	ccttatttgg	ctatgcattt	tttgtataat	tcaatagata	2040
cagtttataa	tggatgtt	ccttacggaa	aattaatgtt	gtgttataat	ggacaagatc	2100
ctgaaataaa	taaagtggaa	aattggttt	aacttcttgc	ttcttgggtt	gataaaaaact	2160
atgtatgtac	tggaggagtt	aatttattt	aatggtaaaa	ctcaatattt	ctatataatt	2220
atgtatattt	ataaaattt	tattcaactt	aaaacttcttgc	cctcaatctt	gaaaatttgc	2280
tttcttaattt	gaggcaatatt	ttaataattt	catttcttgc	tttcaactt	tcttcttattt	2340
aaactgcttt	ttgtctatgt	aaacaataga	tgcttcaaca	attagtattt	ctcctataat	2400
agaatataaca	gataaaagctt	ctccaaataaa	aataaatttttcc	caagcggatt	aaacaatattt	2460
ccttatatttt	acaacttctt	caatttactgc	attagcattt	ccgaaagcac	ctgtttaagaa	2520
tatttgcgt	aataaggaaa	ccgcacccaa	caagattaac	aggattaattt	cttttgcgtt	2580
tgttatttca	aagtttattt	tcatcaatac	tccagcaact	atagtagatg	cagctttagaa	2640
ataaaacactt	atttcgtaat	gatgtatgtt	cttagacttt	gctaatttttgc	ttatggtaat	2700
tgaaggactt	gccgataaaa	ctgcactttaa	catccaaaga	tggcatagaa	agaataagta	2760
gagtatct						2768

11

ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
----------------------------------	--------------------------	-------------------------------	----------------------------	----------------------------

Search	Swiss-Prot/TrEMBL	for	clostripain	<input type="button" value="Go"/>	<input type="button" value="Clear"/>
--------	-------------------	-----	-------------	-----------------------------------	--------------------------------------

NiceProt

View of

Swiss-Prot:

P09870

[Printer-friendly view](#)
[Submit update](#)
[Quick BlastP search](#)

[\[Entry info\]](#)
[\[Name and origin\]](#)
[\[References\]](#)
[\[Comments\]](#)
[\[Cross-references\]](#)
[\[Keywords\]](#)
[\[Features\]](#)
[\[Sequence\]](#)
[\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	CLOS_CLOHI
Primary accession number	P09870
Secondary accession number	P09869
Entered in Swiss-Prot in	Release 10, March 1989
Sequence was last modified in	Release 26, July 1993
Annotations were last modified in	Release 45, October 2004

Name and origin of the protein

Protein name	Alpha-clostripain [Precursor]
Synonyms	EC 3.4.22.8 Clostridiopeptidase B Name: cloSI
Gene name	
From	Clostridium histolyticum [TaxID: 1498]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

[1] NUCLEOTIDE SEQUENCE.

MEDLINE=93341452;PubMed=8341259 [NCBI, ExPASy, EBI, Israel, Japan]
 Dargatz H., Diefenthal T., Witte V., Reipen G., von Wettstein D.;
 "The heterodimeric protease clostripain from Clostridium histolyticum is encoded by a single gene.";
 Mol. Gen. Genet. 240:140-145(1993).

[2] PROTEIN SEQUENCE OF 51-181.

MEDLINE=85076641;PubMed=6391922 [NCBI, ExPASy, EBI, Israel, Japan]
 Gilles A.M., Lecroisey A., Keil B.;
 "Primary structure of alpha-clostripain light chain.";
 Eur. J. Biochem. 145:469-476(1984).

[3] PRELIMINARY PROTEIN SEQUENCE OF 51-73 AND 191-232.

MEDLINE=83131688;PubMed=6337850 [NCBI, ExPASy, EBI, Israel, Japan]
 Gilles A.M., de Wolf A., Keil B. ;

"Amino-acid sequences of the active-site sulphydryl peptide and other thiol peptides from the cysteine proteinase alpha-clostripain.";
Eur. J. Biochem. 130:473-479(1983).

Comments

- **FUNCTION:** Cysteine endopeptidase with strict specificity.
- **CATALYTIC ACTIVITY:** Preferential cleavage: Arg-|-Xaa, including Arg-|-Pro bond, but not Lys-|-Xaa.
- **SUBUNIT:** Heterodimer of a light chain and an heavy chain held together by strong noncovalent forces rather than by intramolecular disulfide bridges.
- **SIMILARITY:** Belongs to the peptidase C11 family [view classification].
- **DATABASE:** NAME=Worthington enzyme manual; WWW="http://www.worthington-biochem.com/CP/".

Copyright

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

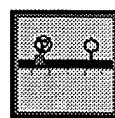
Cross-references

EMBL	X63673; CAA45212.1; -.[EMBL / GenBank / DDBJ] [CoCodingSequence] A29174; A29174.
PIR	A29175; A29175. B29175; B29175. S35190; S35190.
MEROPS	C11.001; -.
InterPro	IPR005077; Peptidase_C11. Graphical view of domain structure.
Pfam	PF03415; Peptidase_C11; 1. Pfam graphical view of domain structure.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P09870.
ProtoNet	P09870.
ProtoMap	P09870.
PRESAGE	P09870.
DIP	P09870.
ModBase	P09870.
SMR	P09870; E151372FF6C95BE7.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

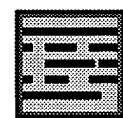
Keywords

Direct protein sequencing; Hydrolase; Signal; Thiol protease; Zymogen.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description
SIGNAL	1	27	27	Potential.

PROPEP	28	50	23	Potential.
CHAIN	51	181	131	Alpha-clostripain light chain.
PEPTIDE	182	190	9	Linker.
CHAIN	191	526	336	Alpha-clostripain heavy chain.
ACT_SITE	231	231		
CONFLICT	127	127		R -> NQL (in Ref. 2).
CONFLICT	176	179		HGGG -> GDGH (in Ref. 2).
CONFLICT	197	197		S -> H (in Ref. 3).
CONFLICT	213	213		I -> L (in Ref. 3).
CONFLICT	216	216		H -> T (in Ref. 3).
CONFLICT	232	232		L -> M (in Ref. 3).

Sequence information

Length: **526 AA** [This is the length of the unprocessed precursor]

Molecular weight: **59733 Da**
[This is the MW of the unprocessed precursor]

CRC64: **E151372FF6C95BE7** [This is a checksum on the sequence]

10	20	30	40	50	60
MLRRKVSTLL	MTALITTSFL	NSKPVYANPV	TKSKDNNLKE	VQQVTSKSNK	NKNQKVTIMY
70	80	90	100	110	120
YCDADNNLEG	SLLNDIEEMK	TGYKDSPNLN	LIALVDRSPR	YSSDEKVLGE	DFSDTRILYKI
130	140	150	160	170	180
EHNKANRLDG	KNEFPEISTT	SKYEANMGDP	EVLKKFIDYC	KSNYEADKYV	LIMANHGGGA
190	200	210	220	230	240
REKSNPRLNR	AICWDDSNLD	KNGEADCLYM	GEISDHLTEK	QSVDLLAFDA	CLMGTAEVAY
250	260	270	280	290	300
QYRPNGGGFS	ADTLVASSPV	VWGPGFKYDK	IFDRIKAGGG	TNNEDDLTLG	GKEQNFDPAT
310	320	330	340	350	360
ITNEQLGALF	VEEQRDSTHA	NGRYDQHLSF	YDLKKAESVK	RAIDNLAVNL	SNENKKSEIE
370	380	390	400	410	420
KLRGSGIHTD	LMHYFDEYSE	GEWVEYPYFD	VYDLCEKINK	SENFSSKTKD	LASNAMNKLN
430	440	450	460	470	480
EMIVYSFGDP	SNNFKEGKNG	LSIFLPNGDK	KYSTYYTSTK	IPHWTMOSWY	NSIDTVKYGL
490	500	510	520		
NPYGKLSWCK	DGQDPEINKV	GNWFELLDW	FDKTNDVTGG	VNHYQW	

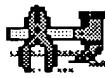
P09870 in FASTA format

[View entry in original Swiss-Prot format](#)

[View entry in raw text format \(no links\)](#)

[Report form for errors/updates in this Swiss-Prot entry](#)

BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository



ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
Hosted by NCSC US	Mirror sites:	Australia	Bolivia	Brazil <small>new</small>

*File 399: Use is subject to the terms of your user/customer agreement.

Alert feature enhanced for multiple files, etc. See HELP ALERT.

File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec

(c) 1998 Inst for Sci Info

*File 434: Price change effective Jan 1, 2005. Enter HELP

RATES 434 for details.

File 444:New England Journal of Med. 1985-2005/Feb W1

(c) 2005 Mass. Med. Soc.

File 467:ExtraMED(tm) 2000/Dec

(c) 2001 Informania Ltd.

*File 467: F467 no longer updates; see Help News467.

7.

Set Items Description

--- -----

Cost is in DialUnits

?ds

Set Items Description

S1 16 AU=DARGATZ ? AND PY=1993

S2 4 S1 AND HISTOLYTICUM?

?t s2/9/1

2/9/1 (Item 1 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2005 The Dialog Corp. All rts. reserv.

09780560 PMID: 8341259

The heterodimeric protease clostripain from Clostridium histolyticum is encoded by a single gene.

Dargatz H ; Diefenthal T; Witte V; Reipen G; von Wettstein D

Weissheimer Research Laboratory, Andernach, Germany.

Molecular & general genetics - MGG (GERMANY) Jul 1993 , 240 (1)
p140-5, ISSN 0026-8925 Journal Code: 0125036

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Clostripain (EC 3.4.22.8) is a heterodimeric cysteine endopeptidase with strict specificity for Arg-Xaa peptidyl bonds. It is secreted by *Clostridium histolyticum* strains. For the first time we present evidence that both polypeptide chains of native clostripain are encoded by a single gene. DNA sequencing of two overlapping genomic DNA fragments revealed a single open reading frame (ORF) of 1581 nucleotides encoding a polypeptide of 526 amino acid residues. The ORF is preceded by canonical transcription signals and both chains of the clostripain heterodimer are completely represented by the deduced coding sequence. Most interestingly, the sequences coding for the light and the heavy chain are joined by a DNA stretch coding for a linker nonapeptide that is preceded by the C-terminal arginyl residue of the light chain and also ends with an arginyl residue. Heterologous expression of the gene in *Escherichia coli* yielded an enzyme capable of hydrolyzing the clostripain substrates N-alpha-benzoyl-L-arginine ethyl ester (BAEE) and N-carbobenzoxy-L-arginine p-nitroanilide (Z-Arg-pNA).

Tags: Support, Non-U.S. Gov't

Descriptors: *Clostridium--enzymology--EN; *Cysteine Endopeptidases--genetics--GE; *DNA, Bacterial--genetics--GE; *Genes, Bacterial--genetics--GE; Amino Acid Sequence; Base Sequence; Clostridium--genetics--GE; Cysteine Endopeptidases--isolation and purification--IP; Escherichia coli; Gene Expression--genetics--GE; Molecular Sequence Data; Protein Sorting Signals--genetics--GE; Transcription, Genetic--genetics--GE

Molecular Sequence Databank No.: GENBANK/X63673

CAS Registry No.: 0 (DNA, Bacterial); 0 (Protein Sorting Signals)

Enzyme No.: EC 3.4.22 (Cysteine Endopeptidases); EC 3.4.22.8 (clostripain)

Record Date Created: 19930902

Record Date Completed: 19930902